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FILE 'HOME' ENTERED AT 16:31:17 ON 24 APR 2001

=> file caplus

=> s microsphere?
L1         16767 MICROSPHERE?

=> s l1 (s) (DNA? or nucleic acid? or oligonucleotide? or polynucleotide?)
          516678 DNA?
          106479 NUCLEIC
         3539006 ACID?
          105674 NUCLEIC ACID?
                   (NUCLEIC(W)ACID?)
           49006 OLIGONUCLEOTIDE?
           13477 POLYNUCLEOTIDE?
L2           205 L1 (S) (DNA? OR NUCLEIC ACID? OR OLIGONUCLEOTIDE? OR POLYNUCLEO
                 IDE?)

=> s l2 (p) (microtiter or micrototre)
            5627 MICROTITER
               0 MICROTOTRE
L3             0 L2 (P) (MICROTITER OR MICROTOTRE)

=> s l2 (p) well?
         1195561 WELL?
L4            19 L2 (P) WELL?

=> s l2 (p) array?
           74088 ARRAY?
L5            17 L2 (P) ARRAY?

=> d ibib 5,6,8 l4



L4   ANSWER 8 OF 19  CAPLUS  COPYRIGHT 2001 ACS
ACCESSION NUMBER:         2000:73909  CAPLUS
DOCUMENT NUMBER:          132:261123
TITLE:                    Techview: Molecular biology: Bead-based fiber-optic
                          arrays
AUTHOR(S):                Walt, David R.
CORPORATE SOURCE:         Dep. Chem., Tufts Univ., Medford, MA, 02155, USA
SOURCE:                   Science (Washington, D. C.) (2000), 287(5452), 451-45
                          CODEN: SCIEAS; ISSN: 0036-8075
PUBLISHER:                American Association for the Advancement of Science
DOCUMENT TYPE:            Journal; General Review
LANGUAGE:                 English
REFERENCE COUNT:          26
REFERENCE(S):             (1) Abel, A; Anal Chem 1996, V68, P2905 CAPLUS
                          (3) Blanchard, A; Biosens and Bioelectron 1996, V11,
                              P687 CAPLUS
                          (5) Case-Green, S; Curr Opin Chem Biol 1998, V2, P404
                              CAPLUS
                          (8) Elghanian, R; Science 1997, V277, P1078 CAPLUS
                          (9) Ferguson, J; Nature Biotechnol 1996, V14, P1681
                              CAPLUS
                          ALL CITATIONS AVAILABLE IN THE RE FORMAT


=> d ibib abs 2-17 l5
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L5 ANSWER 2 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2001:152872 CAPLUS
DOCUMENT NUMBER: 134:203076
TITLE: Liquid array technology
INVENTOR(S): Chandler, Mark B.
PATENT ASSIGNEE(S): Luminex Corporation, USA
SOURCE: PCT Int. Appl., 62 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001014589	A2	20010301	WO 2000-US22769	20000821

PRIORITY APPLN. INFO.: US 1999-149710 P 19990820
AB This invention is directed to compns. and methods of screening, sequencing, and/or quantitating a nucleic acid of interest by hybridizing that nucleic acid with a set of oligonucleotide probes, which are coupled to fluorescently addressable multicolored microparticles. These microparticles are provided as a liq. array that can be positioned in predetd. wells or reaction vessels of a microtiter plate. For sequencing purposes, each such liq. array preferably comprises every possible combination of sequences for a given length of a probe. Hybridization occurs by complementary recognition of the analyte of interest with a probe. Probe, target, and/or competing mol. are tagged with a reporter mol. so that upon hybridization, the changes in fluorescence signal parameters are recorded and analyzed.

L5 ANSWER 4 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:881358 CAPLUS
DOCUMENT NUMBER: 134:39138
TITLE: Combinatorial decoding of random nucleic acid arrays
INVENTOR(S): Walt, David R.
PATENT ASSIGNEE(S): Illumina, Inc., USA
SOURCE: PCT Int. Appl., 78 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000075373	A2	20001214	WO 2000-US13753	20000519

PRIORITY APPLN. INFO.: US 1999-135052 P 19990520
AB The invention relates to compns. and methods for combinatorially decoding microsphere array sensors. It provides array compns. comprising a substrate with a surface comprising discrete sites. The compn. further comprises a population of microspheres comprising at least a first and a second subpopulation; each subpopulation comprises a bioactive agent; and an identifier binding ligand that will bind a decoder binding ligand such that the identity of the bioactive agent can be elucidated. The microspheres are distributed on the surface. The microspheres comprise a least a first and a second subpopulation each comprising a bioactive agen and do not comprise an optical signature. The microspheres comprise at least a first and a second subpopulation each comprising a bioactive agen and an identifier nucleotide sequence comprising a primer sequence and a decoding sequence. The invention provides methods of decoding an array

compn. comprising providing an array compn., and adding a plurality of decoding probes comprising a priming sequence, a decoding sequence, and a label, to the array compn. to identify the location of at least a plurality of the bioactive agents. Reagent kits contg. a plurality of nucleic acids with an invariant and a variable sequence is claimed. Each unique nucleotide at the decoding position within a variable sequence has a different label. Use of probes labeled with dyes, Cy5, Cy3, fluorescein, or Biotin, and attached to beads, is described.

L5 ANSWER 5 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:842042 CAPLUS
DOCUMENT NUMBER: 134:2308
TITLE: The use of microfluidic systems in the detection of target analytes using microsphere arrays
INVENTOR(S): Stuelpnagel, John R.; Chee, Mark S.; Gunderson, Kevin
PATENT ASSIGNEE(S): Illumina, Inc., USA
SOURCE: PCT Int. Appl., 79 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000071243	A1	20001130	WO 2000-US13942	20000522

PRIORITY APPLN. INFO.: US 1999-316154 A 19990521
AB The invention relates generally to methods and app. for conducting analyses, particularly microfluidic devices for the detection of target analytes. The detection modules of the microfluidic devices described herein are based on previous work comprising a bead-based analytic chem. system in which beads, also termed microspheres, carrying chem. functionalities are distributed on an array substrate comprising a patterned surface of discrete sites that can bind the individual microspheres. The beads are generally put onto the substrate randomly, and thus several different methodologies can be used to "decode" the arrays. In one embodiment, unique optical signatures are incorporateed into the beads, generally fluorescent dyes, that could be used to identif the chem. functionality on any particular bead. This allows the synthesi of the candidate agents (i.e. compds. such as nucleic acids and antibodies) to be divorced from their placement on an array, i.e. the candidate agents may be synthesized on the beads, and then the beads are randomly distributed on a patterned surface.
REFERENCE COUNT: 6
REFERENCE(S): (2) Tu, E; US 5632957 A 1997 CAPLUS
(3) Tufts College; WO 9840726 A 1998 CAPLUS
(4) Univ Texas; WO 0004372 A 2000 CAPLUS
(5) Walt, D; US 5244636 A 1993 CAPLUS
(6) Wilding, P; US 5726026 A 1998 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 6 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:756917 CAPLUS
DOCUMENT NUMBER: 133:306332
TITLE: Detection of ***nucleic*** ***acid*** reactions on ***microsphere*** or bead ***arrays***
INVENTOR(S): Gunderson, Kevin; Stuelpnagel, John R.; Chee, Mark S.
PATENT ASSIGNEE(S): Illumina, Inc., USA
SOURCE: PCT Int. Appl., 161 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent

LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000063437	A2	20001026	WO 2000-US10716	20000420

AB The present invention is directed to methods and compns. for the use of ***microsphere*** ***arrays*** to detect and quantify a no. of ***nucleic*** ***acid*** reactions. The methods comprise providi a hybridization complex comprising the target sequence and a capture prob covalently attached to a microsphere on a surface of a substrate. The hybridization complex can comprise the capture probe, a capture extender probe, and the target sequence. The invention finds use in genotyping, i.e. the detn. of the sequence of nucleic acids, particularly alterations such as nucleotide substitutions (mismatches) and single nucleotide polymorphisms (SNPs). Similarly, the invention finds use in the detectio and quantification of a nucleic acid target using a variety of amplification techniques, including both signal amplification and target amplification. The methods and compns. of the invention can be used in nucleic acid sequencing reactions as well. All applications can include the use of adapter sequences to allow for universal ***arrays*** .

L5 ANSWER 7 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:726029 CAPLUS
DOCUMENT NUMBER: 134:68196
TITLE: High-Density Fiber-Optic ***DNA*** Random ***Microsphere*** ***Array***
AUTHOR(S): Ferguson, Jane A.; Steemers, Frank J.; Walt, David R.
CORPORATE SOURCE: Max Tishler Laboratory for Organic Chemistry Department of Chemistry, Tufts University, Medford, MA, 02155, USA
SOURCE: Anal. Chem. (2000), 72(22), 5618-5624
CODEN: ANCHAM; ISSN: 0003-2700
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A high-d. fiber-optic DNA microarray sensor was developed to monitor multiple DNA sequences in parallel. Microarrays were prepd. by randomly distributing ***DNA*** probe-functionalized 3.1-.mu.m-diam. ***microspheres*** in an ***array*** of wells etched in a 500-.mu.m-diam. optical imaging fiber. Registration of the microspheres was performed using an optical encoding scheme and a custom-built imaging system. Hybridization was visualized using fluorescent-labeled DNA targets with a detection limit of 10 fM. Hybridization times of seconds are required for nanomolar target concns., and anal. is performed in minutes.
REFERENCE COUNT: 33
REFERENCE(S):
(1) Baba, Y; J Chromatogr, B: Biomed Appl 1996, V687, P271 CAPLUS
(3) Bronk, K; Anal Chem 1995, V67, P2750 CAPLUS
(5) Chee, M; Science 1996, V274, P610 CAPLUS
(6) Cronin, M; Hum Mutat 1996, V7, P244 CAPLUS
(7) Czarnik, A; Curr Opin Chem Biol 1997, V1, P60 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 8 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:725840 CAPLUS
DOCUMENT NUMBER: 133:305132
TITLE: Self-encoding sensor with microspheres

INVENTOR(S): Walt, David R.; Dickinson, Todd A.
PATENT ASSIGNEE(S): Trustees of Tufts College, US
SOURCE: PCT Int. Appl., 99 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000060332	A2	20001012	WO 2000-US9183	20000406

PRIORITY APPLN. INFO.: US 1999-287573 A 19990406

AB A microsphere-based analytic chem. system is disclosed in which self-encoding microspheres having distinct characteristic optical respons signatures to specific target analytes may be mixed together while the ability is retained to identify the sensor type and location of each sensor in a random dispersion of large nos. of such sensors in a sensor array using an optically interrogatable encoding scheme. An optical fibe bundle sensor is also disclosed in which individual microsphere sensors are disposed in microwells at a distal end of the fiber bundle and are optically coupled to discrete fibers or groups of fibers within the bundle. The identities of the individual sensors in the array are self-encoded by exposing the array to a ref. analyte while illuminating the array with excitation light energy. A single sensor array may carry thousands of discrete sensing elements whose combined signal provides for substantial improvements in sensor detection limits, response times and signal-to-noise ratios.

L5 ANSWER 13 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:457254 CAPLUS
DOCUMENT NUMBER: 133:85099
TITLE: Aldehyde-linker-based ultrasensitive mismatch scannin (ALBUMS) using mutation scanning array
INVENTOR(S): Makrigiorgos, G. Mike
PATENT ASSIGNEE(S): Dana-Farber Cancer Institute, Inc., USA
SOURCE: PCT Int. Appl., 76 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000039345	A1	20000706	WO 1999-US31177	19991229

W: AU, CA, JP, US
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

PRIORITY APPLN. INFO.: US 1998-114196 P 19981230
OTHER SOURCE(S): MARPAT 133:85099

AB The present method is directed to using a mutation scanning array to identify mismatches or polymorphisms in multiple genes or the same gene i multiple individuals. The array can be a chip or a microsphere. Preferably, the array has elements contg. immobilized oligonucleotides that collectively span at least 10 different whole genes. Genes known to predispose an individual to a particular disease are selected to be analyzed. The target DNA sequence is hybridized with a control DNA sequence wherein said control DNA sequence is the wild-type DNA sequence corresponding to the target DNA sequence to create a duplex. The duplex is treated with hydroxylamine to remove any spontaneous aldehydes, and

reacted with a repair glycosylase to convert any mismatched sites in the duplex to reactive sites contg. an aldehyde-contg. abasic site. The duplex is then reacted with a labeling compd. of the formula X-Z-Y, wherein X is a detectable moiety, Y is NHNH2, O-NH2 or NH2, and Z is a hydrocarbon, alkylhydroxy, alkylethoxy, alkylester, alkylether, alkylamid or alkylamine, wherein Z may be substituted or unsubstituted; and wherein Z may contain a cleavable group; for a sufficient time and under conditions to covalently bind to the reactive sites. The bound compd. is detected to identify sites of mismatches, where the mismatch occurs is detd., whether the mismatch is a mutation or polymorphisms is detd. Suitable abasic site-reactive reagents include 2-(aminoacetylamino)ethylenediamine (AED), FARP (a fluoresceinated hydroxylamine-contg. compd.), and BARP (a biotinylated hydroxylamine-contg. compd.). Suitable mismatch repair enzymes include MutY and thymine DNA glycosidase.

REFERENCE COUNT: 9

REFERENCE(S):
(1) Affymetrix Inc; WO 9830883 1998 CAPLUS
(2) Asaeda, A; Analytica Chimica Acta 1998, V365, P35 CAPLUS
(3) Boturyn; Tetrahedron 1997, V53(15), P5485 CAPLUS
(4) Fulton; US 5736330 A 1998 CAPLUS
(5) Gelfand; US 5418149 A 1995 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 14 OF 17 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2000:406810 CAPLUS

DOCUMENT NUMBER: 134:158204

TITLE: Suspension arrays for high throughput, multiplexed single nucleotide polymorphism genotyping

AUTHOR(S): Armstrong, Barbara; Stewart, Michael; Mazumder, Abhijit

CORPORATE SOURCE: Axys Pharmaceuticals, La Jolla, CA, USA

SOURCE: Cytometry (2000), 40(2), 102-108
CODEN: CYTODQ; ISSN: 0196-4763

PUBLISHER: Wiley-Liss, Inc.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Genetic diversity can help explain disease susceptibility and differentia drug response. The most common type of variant is the single nucleotide polymorphism (SNP). We present a low-cost, high throughput assay for SNP genotyping. The assay uses ***oligonucleotide*** probes covalently attached to fluorescently encoded ***microspheres*** . These probes are hybridized directly to fluorescently labeled polymerase chain reactio (PCR) products and the results are analyzed in a std. flow cytometer. Th genotypes detd. with our assay are in good agreement with those detd. by TaqMan. The range of G/C content for oligonucleotide probes was 23.5-65% in the 17 bases surrounding the SNP. Further optimization of probe lengt and target concn. is shown to dramatically enhance the assay performance for certain SNPs. Using microspheres which have unique fluorescent signatures, we performed a 32-plex assay where we simultaneously detd. th genotypes of eight different polymorphic genes. We demonstrate, for the first time, the feasibility of multiplexed genotyping with suspension ***arrays*** using direct hybridization analyses. Our approach enabl probes to be removed from or added to an ***array*** , enhancing flexibility over conventional chips. The ability to multiplex both the PCR prepn. and the hybridization should enhance the throughput, cost, and speed of the assay.

REFERENCE COUNT: 20

REFERENCE(S):
(1) Ahn, S; Nucleic Acids Res 1996, V24, P2623 CAPLUS
(2) Bailey, D; Curr Opin Biotechnol 1998, V9, P595 CAPLUS
(3) Chee, M; Science 1996, V274, P610 CAPLUS
(4) Collins, F; Science 1997, V278, P1580 CAPLUS

(5) Cooper, D; Hum Genet 1985, V69, P201 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 15 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:306823 CAPLUS
DOCUMENT NUMBER: 133:218244
TITLE: A microsphere-based assay for multiplexed single nucleotide polymorphism analysis using single base chain extension
AUTHOR(S): Chen, Jingwen; Iannone, Marie A.; Li, May-Sung; Taylor, J. David; Rivers, Philip; Nelsen, Anita J.; Slentz-Kesler, Kimberly A.; Roses, Allen; Weiner, Michael P.
CORPORATE SOURCE: Department of Genomic Sciences, Glaxo Wellcome Research and Development, Research Triangle Park, NC, 27709-3398, USA
SOURCE: Genome Res. (2000), 10(4), 549-557
CODEN: GEREFS; ISSN: 1088-9051
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A rapid, high throughput readout for single-nucleotide polymorphism (SNP) anal. was developed employing single base chain extension and cytometric anal. of an ***array*** of fluorescent microspheres. An ***array** of fluorescent microspheres was coupled with uniquely identifying sequences, termed complementary ZipCodes (cZipCodes), which allowed for multiplexing possibilities. For a given assay, querying a polymorphic base involved extending an oligonucleotide contg. both a ZipCode and a SNP-specific sequence with a DNA polymerase and a pair of fluoresceinated dideoxynucleotides. To capture the reaction products for anal., the ZipCode portion of the ***oligonucleotide*** was hybridized with its cZipCodes on the ***microsphere*** . Flow cytometry was used for microsphere decoding and SNP typing by detecting the fluorescein label captured on the microspheres. In addn. to multiplexing capability, the ZipCode system allows multiple sets of SNPs to be analyzed by a limited set of cZipCode-attached microspheres. A std. set of non-cross reactive ZipCodes was established exptl. and the accuracy of the system was validated by comparison with genotypes detd. by other technologies. From a total of 58 SNPs, 55 SNPs were successfully analyzed in the first pass using this assay format and all 181 genotypes across the 55 SNPs were correct. These data demonstrate that the microsphere-based single base chain extension (SBCE) method is a sensitive and reliable assay. It can be readily adapted to an automated, high-throughput genotyping system.
REFERENCE COUNT: 24
REFERENCE(S): (1) Chen, X; Genome Res 1999, V9, P492 CAPLUS
(2) Chen, X; Proc Natl Acad Sci 1997, V94, P10756 CAPLUS
(3) Cooper, D; Hum Genet 1985, V69, P201 CAPLUS
(4) Fu, D; Nat Biotechnol 1998, V16, P381 CAPLUS
(5) Fulton, R; Clin Chem 1997, V43, P1749 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 16 OF 17 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:73909 CAPLUS
DOCUMENT NUMBER: 132:261123
TITLE: Techview: Molecular biology: Bead-based fiber-optic arrays
AUTHOR(S): Walt, David R.
CORPORATE SOURCE: Dep. Chem., Tufts Univ., Medford, MA, 02155, USA
SOURCE: Science (Washington, D. C.) (2000), 287(5452), 451-45
CODEN: SCIEAS; ISSN: 0036-8075
PUBLISHER: American Association for the Advancement of Science
DOCUMENT TYPE: Journal; General Review

LANGUAGE: English

AB A review with 26 refs. on the application of fiber-optic technol. to bead-based DNA hybridization. Imaging optical fibers each contain an ***array*** of individual fibers, each of which can carry its own lig signal. The distal end of each component fiber's core can be selectively etched to create an ***array*** of wells on the end of the composite imaging optical fiber. ***DNA*** probes are attached to ***microspheres*** of latex or silica, then the ***microspheres*** are deposited in the ***arrays*** of wells on the imaging optical fiber. Hybridization of fluorescently labeled DNA mols. to the ***array*** generate signals that can captured by a CCD camera.

REFERENCE COUNT: 26

REFERENCE(S):

(1) Abel, A; Anal Chem 1996, V68, P2905 CAPLUS
(3) Blanchard, A; Biosens and Bioelectron 1996, V11, P687 CAPLUS
(5) Case-Green, S; Curr Opin Chem Biol 1998, V2, P404 CAPLUS
(8) Elghanian, R; Science 1997, V277, P1078 CAPLUS
(9) Ferguson, J; Nature Biotechnol 1996, V14, P1681 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 17 OF 17 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1999:819573 CAPLUS
DOCUMENT NUMBER: 132:32909
TITLE: Decoding of array sensors with microspheres
INVENTOR(S): Chee, Mark S.; Stuelpnagel, John R.; Czarnik, Anthony W.
PATENT ASSIGNEE(S): Illumina, Inc., USA
SOURCE: PCT Int. Appl., 43 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9967641	A2	19991229	WO 1999-US14387	19990624
WO 9967641	A3	20000309		
AU 9948315	A1	20000110	AU 1999-48315	19990624
EP 1090293	A2	20010411	EP 1999-931904	19990624

AB The invention relates to compns. and methods for decoding microsphere array sensors. It provides array compns. comprising a substate with a surface comprising discrete sites. The compn. further comprises a population of microspheres comprising at least a first and a second subpopulation; each subpopulation comprises a bioactive agent; and an identifier binding ligand that will bind a decoder binding ligand such that the identity of the bioactive agent can be elucidated. The microspheres are distributed on the surface. The microspheres comprise a least a first and a second subpopulation each comprising a bioactive agen and do not comprise an optical signature. The microspheres comprise at least a first and a second subpopulation each comprising a bioactive agen and an identifier binding ligand that will bind a decoder binding ligand such that the identification of the bioactive agent can be elucidated. The invention provides methods of decoding an array compn. comprising providing an array compn., and adding a plurality of decoding binding ligands to the array compn. to identify the location of at least a plurality of the bioactive agents. Bioactive agents are proteins or nucleic acids.

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L1 32 CHEE M?/IN

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17442092 PY<1999
L2 16 L1 AND PY<1999

=> d ibib abs

L2 ANSWER 1 OF 16 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:858567 CAPLUS
DOCUMENT NUMBER: 134:26053
TITLE: Oligonucleotide analog probe arrays immobilized on solid substrates, target nucleic acid analogs, and probe-target improved hybridization
INVENTOR(S): McGall, Glenn Hugh; Miyada, Charles Garrett; Cronin, Maureen T.; Tan, Jennifer Dee; ***Chee, Mark S.***
PATENT ASSIGNEE(S): Affymetrix, Inc., USA
SOURCE: U.S., 35 pp., Cont.-in-part of U.S. Ser. No. 440,742, abandoned.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 7
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
US 6156501	A	20001205	US 1996-630427	19960403	
WO 9511995	A1	19950504	WO 1994-US12305	19941026	<--
US 5837832	A	19981117	US 1995-441887	19950516	<--
EP 742287	A2	19961113	EP 1996-303245	19960509	<--
EP 742287	A3	19971229			
R: DE, FR, GB, IT, NL					
US 5861242	A	19990119	US 1997-781550	19970109	

OTHER SOURCE(S): MARPAT 134:26053
AB Oligonucleotide analog arrays attached to solid substrates and methods related to the use thereof are provided. The oligonucleotide analogs hybridize to nucleic acids with either higher or lower specificity than corresponding unmodified oligonucleotides. Target nucleic acids which comprise nucleotide analogs are bound to oligonucleotide and oligonucleotide analog arrays. Examples include oligonucleotide probe arrays synthesized using VLSIPS (very large scale immobilized polymer synthesis), amplification of nucleic acid targets with incorporation of nucleotide analogs, and probe-target duplex thermostability anal.
REFERENCE COUNT: 22
REFERENCE(S): (1) Anon; WO 8605518 1986 CAPLUS
(2) Anon; WO 8910977 1989 CAPLUS
(3) Anon; WO 8911548 1989 CAPLUS
(4) Anon; WO 9004652 1990 CAPLUS

(5) Anon; WO 9210092 1992 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d ibib abs 2-16

L2 ANSWER 2 OF 16 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:124057 CAPLUS
DOCUMENT NUMBER: 132:176568
TITLE: Arrays of nucleic acid probes and the detection of cystic fibrosis carriers or patients by sequencing by hybridization
INVENTOR(S): Cronin, Maureen T.; Miyada, Charles Garrett; Hubbell, Earl A.; ***Chee, Mark*** ; Fodor, Stephen P. A.; Huang, Xiaohua C.; Lipshutz, Robert J.; Lobban, Peter E.; Morris, Macdonald S.; Sheldon, Edward L.
PATENT ASSIGNEE(S): Affymetrix, Inc., USA
SOURCE: U.S., 114 pp., Cont.-in-part of U.S. Ser. No. 510,521
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 7
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
US 6027880	A	20000222	US 1995-544381	19951010	
WO 9511995	A1	19950504	WO 1994-US12305	19941026	<--
US 5837832	A	19981117	US 1995-441887	19950516	<--
US 6045996	A	20000404	US 1996-648709	19960516	
US 5861242	A	19990119	US 1997-781550	19970109	

AB Organized arrays of immobilized probes that can be used to rapidly sequence the CFTR gene and to detect mutations in carriers or in the diagnosis of patients are described. The arrays consist of several lanes with one carrying an array of overlapping probes corresponding to the wild-type gene. The other lanes contain similar arrays of probes with their sequences systematically altered, one lane is dedicated to substitutions with one base.
REFERENCE COUNT: 20
REFERENCE(S): (1) Anon; WO 8910977 1989 CAPLUS
(2) Anon; WO 8911548 1989 CAPLUS
(3) Anon; WO 9000626 1990 CAPLUS
(4) Anon; WO 9003382 1990 CAPLUS
(5) Anon; WO 9210092 1992 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 3 OF 16 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:686783 CAPLUS
DOCUMENT NUMBER: 131:318542
TITLE: Computer-aided visualization and analysis system for nucleic acid sequence evaluation
INVENTOR(S): ***Chee, Mark S.***
PATENT ASSIGNEE(S): Affymetrix, Inc., USA
SOURCE: U.S., 59 pp., Cont.-in-part of U.S. 5,795,716.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

US 5974164	A	19991026	US 1995-5[redacted]137	19951016
US 5795716	A	19980818	US 1994-327525	19941021 <--

PRIORITY APPLN. INFO.: US 1994-327525 19941021

AB A computer system (ViewSeq.RTM.) for analyzing nucleic acid sequences is provided. The computer system is used to perform multiple methods for detg. unknown bases by analyzing the fluorescence intensities of hybridized nucleic acid probes. The results of individual expts. may be improved by processing nucleic acid sequences together. Comparative anal of multiple expts. is also provided by displaying ref. sequences in one area and sample sequences in another area on a display device. This computer system is useful for identifying disease-related gene mutations or virus gene polymorphism.

REFERENCE COUNT: 28

REFERENCE(S):
(1) Anon; WO 89/10977 1989 CAPLUS
(2) Anon; WO 9210588 1991 CAPLUS
(3) Anon; WO 92/10092 1992 CAPLUS
(4) Anon; WO 92/10588 1992 CAPLUS
(5) Anon; WO 95/11995 1995 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 4 OF 16 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1999:42563 CAPLUS

DOCUMENT NUMBER: 130:106006

TITLE: Probes and primers for detection of human genetic polymorphisms and disease diagnosis

INVENTOR(S): Lipshutz, Robert J.; ***Chee, Mark*** ; Fan, Jian Bing; Berno, Anthony

PATENT ASSIGNEE(S): Affymetrix, Inc., USA

SOURCE: PCT Int. Appl., 61 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9858529	A2	19981230	WO 1998-US12930	19980622 <--

PRIORITY APPLN. INFO.: US 1997-50594 19970624

AB Oligonucleotides which can be used as probes for human polymorphisms are disclosed. These probes are based on STS developed in the course of the Human Genome Project. The sequences of the STSs, primers for amplification of the fragments, and the genomic location of the fragments are provided at three Web sites, which are given.

L2 ANSWER 5 OF 16 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1999:8155 CAPLUS

DOCUMENT NUMBER: 130:62005

TITLE: Method to detect gene polymorphisms and monitor allelic expression employing a probe array

INVENTOR(S): ***Chee, Mark***

PATENT ASSIGNEE(S): Affymetrix, Inc., USA

SOURCE: PCT Int. Appl., 30 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

WO 9856954 A1 19981217 WO 1998-US12442 19980611 <--

AB The invention provides methods of monitoring expression levels of different polymorphic forms of a gene. Such methods entail analyzing genomic DNA from an individual to det. the presence of heterozygous polymorphic forms at a polymorphic site within a transcribed sequence of gene of interest. RNA from a tissue of the individual in which the gene is expressed is then analyzed to det. relative proportions of polymorphic forms in transcripts of the gene. Having identified alleles of a gene that are expressed at different levels, the alleles can be further analyzed to locate a second polymorphism that has a causative role in the different expression levels. The methods are amenable to analyzing large collections of genes simultaneously using arrays of immobilized probes.

REFERENCE COUNT: 6
REFERENCE(S):
(1) Apple; US 5567809 A 1996 CAPLUS
(2) Cantor; US 5503980 A 1996 CAPLUS
(3) Cantor; US 5631134 A 1997 CAPLUS
(4) Cantor; US 5795714 A 1998 CAPLUS
(5) Guo, Z; Nucleic Acids Research 1994, V22(24), P5456 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 6 OF 16 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:640369 CAPLUS
DOCUMENT NUMBER: 129:255994
TITLE: Iterative resequencing of polynucleotides using an array of probes
INVENTOR(S): ***Chee, Mark***
PATENT ASSIGNEE(S): Affymetrix, Inc., USA
SOURCE: PCT Int. Appl., 22 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9841657	A1	19980924	WO 1998-US5451	19980319 <--
W: JP, US, US				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, S				
EP 972078	A1	20000119	EP 1998-911860	19980319
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.:
US 1997-41435 P 19970320
US 1998-73853 P 19980202
WO 1998-US5451 W 19980319

AB The invention provides iterative methods of analyzing a target nucleic acid that represents a variant of a ref. nucleic acid. An array of probe is designed to be complementary to an estd. sequence of a target nucleic acid. The array of probes is then hybridized to the target nucleic acid. The target sequence is reestimated from hybridization pattern of the arra to the target nucleic acid. A further array of probes is then designed t be complementary to the reestimated sequence, and this array is used to obtain a further reestimate of the sequence of the target nucleic acid. By performing iterative cycles of array design and target sequence estn., the estd. sequence of the target converges with the true sequence.

L2 ANSWER 7 OF 16 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:493727 CAPLUS
DOCUMENT NUMBER: 129:118762
TITLE: Analysis of genetic polymorphisms and gene copy numbe using oligonucleotide probe arrays

INVENTOR(S): [redacted]onin, Maureen T.; Miyada, [redacted]harles G.; Hubbell, Earl [redacted]; ***Chee, Mark*** ; Fo[redacted]r, Stephen P. A.; Huang Xiaohua C.; Lipshutz, Robert J.; Lobban, Peter E.; Morris, Macdonald S.; Sheldon, Edward L.
PATENT ASSIGNEE(S): Affymetrix, Inc., USA
SOURCE: PCT Int. Appl., 114 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9830883	A2	19980716	WO 1998-US6414	19980102 <--
WO 9830883	A3	19981029		
W: JP, US				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, S				
EP 970251	A2	20000112	EP 1998-947218	19980102
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.: US 1997-778794 19970103
WO 1998-US6414 19980102

AB The invention provides methods for detecting variations in polymorphic sites and/or variations in gene copy no. A no. of strategies for comparing a polynucleotide of known sequence (a ref. sequence) with variants of that sequence (target sequence) are provided. The comparison can be performed at the level of entire genomes, chromosomes, genes, exon or introns, or can focus on individual mutant sites and immediately adjacent bases. The strategies allow detection of variations, such as mutations or polymorphisms, in the target sequence irresp. whether a particular variant has previously been characterized. The strategies bot define the nature of a variant and identify its location in a target sequence. The strategies employ arrays of oligonucleotide probes immobilized to a solid support (DNA chips). Target sequences are analyze by detg. the extent of hybridization at particular probes in the array. The strategy in selection of probes facilitates distinction between perfectly matched probes and probes showing single-base or other degrees of mismatches. The strategies usually entails sampling each nucleotide o interest in a target sequence several times, thereby achieving a high degree of confidence in its identity. This level of confidence is furthe increased by sampling of adjacent nucleotides in the target sequence to nucleotides of interest. The present tiling strategies result in sequencing and comparison methods suitable for routine large-scale practice with a high degree of confidence in the sequence output. The methods are particularly useful for anal. of biotransformation genes, suc as cytochromes P 450, and for screening an animal to tissue for the capacity to metabolize a drug.

L2 ANSWER 8 OF 16 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:293656 CAPLUS
DOCUMENT NUMBER: 129:6733
TITLE: Polymorphisms in the human glucose-6 phosphate dehydrogenase locus
INVENTOR(S): ***Chee, Mark*** ; Fan, Jian-Bing
PATENT ASSIGNEE(S): Affymetrix, Inc., USA; Chee, Mark; Fan, Jian-Bing
SOURCE: PCT Int. Appl., 38 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9818967	A1	19980507	WO 1997-US19665	19971027 <--
US 5856104	A	19990105	US 1997-813508	19970307
AU 9851554	A1	19980522	AU 1998-51554	19971027 <--

PRIORITY APPLN. INFO.:
US 1996-29374 19961028
US 1997-813508 19970307
WO 1997-US19665 19971027

AB The invention provides nucleic acid segments of the glucose-6 phosphate dehydrogenase (G6PD) locus of the human genome including polymorphic sites. Ten polymorphisms are identified in sequence-tagged sites in the human G6PD locus by hybridization to tiling arrays which did not contain repetitive Alu sequences. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic anal.

L2 ANSWER 9 OF 16 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:13735 CAPLUS
DOCUMENT NUMBER: 128:71643
TITLE: Polymorphisms in human mitochondrial nucleic acid
INVENTOR(S): ***Chee, Mark*** ; Berno, Anthony; Yang, Robert
PATENT ASSIGNEE(S): Affymetrix, Inc., USA
SOURCE: Eur. Pat. Appl., 28 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 812922	A2	19971217	EP 1997-303327	19970516 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 10099085	A2	19980421	JP 1997-163203	19970516 <--
US 6207960	B1	20010327	US 1999-295214	19990421

PRIORITY APPLN. INFO.:
US 1996-17203 P 19960516
US 1996-24206 P 19960820
US 1997-856642 A1 19970515

AB The invention provides novel human mitochondrial polymorphisms, and probe and primers for detecting the same. Detection of such polymorphisms is useful in a variety of fields such as forensic anal., epidemiol. and preventive medicine. The sequencing of the complete genome of several individuals resulted in the identification of 505 polymorphisms at 182 sites.

L2 ANSWER 10 OF 16 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:544330 CAPLUS
DOCUMENT NUMBER: 127:201011
TITLE: Oligonucleotide probe arrays immobilized on chips, computer programs for hybridization pattern comparison, and species identification or polymorphis or mutation characterization
INVENTOR(S): Gingeras, Thomas A.; Mack, David; ***Chee, Mark*** S.*** ; Berno, Anthony J.; Stryer, Lubert; Ghan Ghassan; Wang, Ching
PATENT ASSIGNEE(S): Affymetrix, Inc., USA; Gingeras, Thomas A.; Mack, David; Chee, Mark S.; Berno, Anthony J.; Stryer, Lubert; Ghandour, Ghassan; Wang, Ching
SOURCE: PCT Int. Appl., 132 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9729212	A1	19970814	WO 1997-US2102	19970207 <--

AB This invention provides oligonucleotide-based arrays and methods for speciating and phenotyping organisms, for example, using oligonucleotide sequences based on the Mycobacterium tuberculosis rpoB gene. The groups or species to which an organism belongs may be detd. by comparing hybridization patterns of target nucleic acid from the organism to hybridization patterns in a database. An example includes Mycobacterium tuberculosis gene rpoB anal. to identify mutations conferring resistance to rifampicin. A total of 25 M. tuberculosis isolates were analyzed. Seven of these were rifampicin resistant and had mutations. Other than the mutations identified, there were no polymorphisms in any of the 25 isolates. Another example included hybridization patterns (fingerprints) for 7 clin. important Mycobacteria species: M. gordonae, M. chelonae, M. kansasii, M. scrofulaceum, M. avium, M. intracellulare, and M. xenopi.

L2 ANSWER 11 OF 16 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:517576 CAPLUS
DOCUMENT NUMBER: 127:186611
TITLE: Determination of patterns of gene expression by hybridization against dense ordered arrays of arbitrary oligonucleotides
INVENTOR(S): Lockhart, David J.; ***Chee, Mark*** ; Gunderson, Kevin; Lai, Chaoqiang; Wodicka, Lisa; Cronin, Maureen T.; Lee, Danny; Tran, Huu M.; Matsuzaki, Hajime; McGall, Glenn H.; Barone, Anthony D.
PATENT ASSIGNEE(S): Affymetrix, Inc., USA; Lockhart, David J.; Chee, Mark Gunderson, Kevin; Lai, Chaoqiang; Wodicka, Lisa; Cronin, Maureen T.; Lee, Danny; Tran, Huu M.; et al.
SOURCE: PCT Int. Appl., 214 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9727317	A1	19970731	WO 1997-US1603	19970122 <--
AU 9722533	A1	19970820	AU 1997-22533	19970122 <--

PRIORITY APPLN. INFO.: US 1996-10471 19960123
WO 1997-US1603 19970122
OTHER SOURCE(S): MARPAT 127:186611
AB A simplified method for identifying differences in nucleic acid abundance (e.g., expression levels) between two or more samples using an array of a large no. (e.g. > 1,000) of arbitrarily selected different oligonucleotid probes where the sequence and location of each different probe is known. Nucleic acid samples (e.g. mRNA) are hybridized to the probe arrays and the pattern of hybridization is detd. Differences in the hybridization patterns between the samples indicates differences in expression of various genes between those samples. Methods of end-labeling a nucleic acid by ligation of a labeled oligonucleotide to it is also described. These methods can be used to detect hybridization by making end-labeling of the immobilized probe dependent upon formation of a hybrid. For example, if the nucleic acid is an RNA, a labeled oligoribonucleotide can

be ligated using an RNA ligase. End-labeling can also be accomplished by with labeled nucleoside triphosphates, and attaching them to the nucleic acid using a terminal transferase.

L2 ANSWER 12 OF 16 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:283823 CAPLUS
DOCUMENT NUMBER: 126:260132
TITLE: Quantification of level of expression of hundreds to millions of genes using hybridization to high density synthetic oligonucleotide probe arrays immobilized on a surface
INVENTOR(S): Lockhart, David J.; Brown, Eugene L.; Wong, Gordon; ***Chee, Mark*** ; Gingeras, Thomas R.; Mittmann, Michael P.; Lipshutz, Robert J.; Fodor, Stephen P. A. Wang, Chunwei
PATENT ASSIGNEE(S): Affymax Technologies N.V., Neth.; Lockhart, David J.; Brown, Eugene L.; Wong, Gordon; Chee, Mark; Gingeras, Thomas R.; Mittmann, Michael P.; Lipshutz, Robert J.; Fodor, Stephen P. A.; Wang, Chunwei
SOURCE: PCT Int. Appl., 126 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9710365	A1	19970320	WO 1996-US14839	19960913 <--

AB This invention provides methods of monitoring the expression levels of a multiplicity of genes. The methods involve hybridizing a nucleic acid sample to a high d. array of oligonucleotide probes where the high d. array contains oligonucleotide probes complementary to subsequences of target nucleic acids in the nucleic acid sample. In one embodiment, the method involves providing a pool of target nucleic acids comprising RNA transcripts of one or more target genes, or nucleic acids derived from th RNA transcripts, hybridizing said pool of nucleic acids to an array of oligonucleotide probes immobilized on surface, where the array comprising more than 100 different oligonucleotides and each different oligonucleotide is localized in a predetd. region of the surface, the d. of the different oligonucleotides is greater than about 60 different oligonucleotides per 1 cm2, and the oligonucleotide probes are complementary to the RNA transcripts or nucleic acids derived from the RN transcripts; and quantifying the hybridized nucleic acids in the array.

L2 ANSWER 13 OF 16 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:14728 CAPLUS
DOCUMENT NUMBER: 126:43598
TITLE: Oligonucleotide analog probe arrays immobilized on solid substrates, target nucleic acid analogs, and probe-target improved hybridization
INVENTOR(S): Mcgall, Glenn H.; Miyada, Charles G.; Cronin, Maureen T.; Tan, Jennifer D.; ***Chee, Mark S.***
PATENT ASSIGNEE(S): USA
SOURCE: Eur. Pat. Appl., 43 pp
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 7
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

EP 742287	A2	19961113	EP 1996-302245	19960509 <--
EP 742287	A3	19971229		
R: DE, FR, GB, IT, NL				
US 6156501	A	20001205	US 1996-630427	19960403

PRIORITY APPLN. INFO.:
US 1995-440742 A 19950510
US 1996-630427 A 19960403
US 1993-143312 B2 19931026
US 1994-284064 B2 19940802
WO 1994-US12305 A2 19941026

OTHER SOURCE(S): MARPAT 126:43598

AB Oligonucleotide analog arrays attached to solid substrates and methods related to the use thereof are provided. The oligonucleotide analogs hybridize to nucleic acids with either higher or lower specificity than corresponding unmodified oligonucleotides. Target nucleic acids which comprise nucleotide analogs are bound to oligonucleotide and oligonucleotide analog arrays. Examples include oligonucleotide probe arrays synthesized using VLSIPS (very large scale immobilized polymer synthesis), amplification of nucleic acid targets with incorporation of nucleotide analogs, and probe-target duplex thermostability anal.

L2 ANSWER 14 OF 16 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:458126 CAPLUS
DOCUMENT NUMBER: 125:107046
TITLE: Nucleic acid library arrays, methods for synthesizing them and methods for sequencing and sample screening using them
INVENTOR(S): Lockhart, David J.; ***Chee, Mark S.*** ; Vetter, Dirk; Diggelmann, Martin
PATENT ASSIGNEE(S): Affymax Technologies N.V., Neth. Antilles
SOURCE: Eur. Pat. Appl., 73 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 721016	A2	19960710	EP 1995-307501	19951020 <--
EP 721016	A3	19991103		
R: DE, FR, GB, IT, NL				
US 5556752	A	19960917	US 1994-327687	19941024 <--
US 5770722	A	19980623	US 1996-664093	19960613 <--

PRIORITY APPLN. INFO.:
US 1994-327522 19941021
US 1994-327687 19941024
US 1995-533582 19951018

AB Disclosed are methods for discriminating between fully complementary hybrids and those that differ by one or more base pairs and libraries of unimol., double-stranded oligonucleotides on a solid support. In these methods, the quality of hybridization signals on high d. oligonucleotide arrays is improved by (1) the nuclease treatment and (2) ligation reactions. Also provided are libraries of unimol. or intermol., double-stranded oligonucleotides on a solid support. These libraries are useful in pharmaceutical discovery for the screening of numerous biol. samples for specific interactions between the double-stranded oligonucleotides, and peptides, proteins, drugs and RNA. In a related aspect, the present invention provides libraries of conformationally restricted probes on a solid support. The probes are restricted in their movement and flexibility using double-stranded oligonucleotides as scaffolding. The probes are also useful in various screening procedures assocd. with drug discovery and diagnosis. The present invention further provides methods for the prepn. and screening of the above libraries.

L2 ANSWER 15 OF 16 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:452277 CAPLUS
DOCUMENT NUMBER: 125:107029
TITLE: Computer-aided visualization and analysis system for nucleic acid sequence evaluation
INVENTOR(S): ***Chee, Mark S.*** ; Wang, Chunwei; Jevons, Luis C.; Bernhart, Derek H.; Lipshutz, Robert J.
PATENT ASSIGNEE(S): Affymax Technologies N.V., Neth. Antilles
SOURCE: Eur. Pat. Appl., 78 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 717113	A2	19960619	EP 1995-307476	19951020 <--
EP 717113	A3	19960717		
R: DE, FR, GB, IT, NL				
US 5795716	A	19980818	US 1994-327525	19941021 <--

PRIORITY APPLN. INFO.: US 1994-327525 19941021

AB A computer system (1) for analyzing nucleic acid sequences is provided. The computer system is used to perform multiple methods for detg. unknown bases by analyzing the fluorescence intensities of hybridized nucleic aci probes. The results of individual expts. may be improved by processing nucleic acid sequences together. Comparative anal. of multiple expts. is also provided by displaying ref. sequences in one area and sample sequences in another area on a display device. This computer system is useful for identifying disease-related gene mutations or virus gene polymorphism.

L2 ANSWER 16 OF 16 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1995:713926 CAPLUS
DOCUMENT NUMBER: 123:135082
TITLE: Arrays of oligonucleotide probes immobilized on silic chips and selective nucleic acid hybridization for biochemical studies and medical diagnostics
INVENTOR(S): ***Chee, Mark*** ; Cronin, Maureen T.; Fodor, Stephen P. A.; Gingeras, Thomas R.; Huang, Xiaohua C. Hubbell, Earl A.; Lipshutz, Robert J.; Lobban, Peter E.; Miyada, Charles Garrett; et al.
PATENT ASSIGNEE(S): Affymax Technologies N.V., Neth.
SOURCE: PCT Int. Appl., 222 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 7
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9511995	A1	19950504	WO 1994-US12305	19941026 <--

AB The invention provides chips of immobilized oligonucleotide probes, and methods employing the chips, for comparing a ref. polynucleotide sequence of known sequence with a target sequence showing substantial similarity with the ref. sequence, but differing in the presence of e.g., mutations. Human immunodeficiency virus genes, cystic fibrosis genes, and the human mitochondrial genome exemplify uses of the methods.

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=> s stuelpnagel j/in
L3            0 STUELPNAGEL J/IN

=> s stuelpnagel j?/in
L4            8 STUELPNAGEL J?/IN

=> s l4 and py<1999
      17442092 PY<1999
L5            0 L4 AND PY<1999

=> s chee m?/au
L6           71 CHEE M?/AU

=> s l6 and py<1999
      17442092 PY<1999
L7           50 L6 AND PY<1999

=> s l7 and (dna or nucleic acid or oligonucleotide or polynucleotide)
         505849 DNA
         106500 NUCLEIC
        2955456 ACID
          69613 NUCLEIC ACID
                  (NUCLEIC(W)ACID)
          34173 OLIGONUCLEOTIDE
           8811 POLYNUCLEOTIDE
L8           34 L7 AND (DNA OR NUCLEIC ACID OR OLIGONUCLEOTIDE OR POLYNUCLEOTID
                E)

=> s l8 and array?
          74102 ARRAY?
L9           18 L8 AND ARRAY?

=> d ibib abs tot

L9   ANSWER 1 OF 18  CAPLUS  COPYRIGHT 2001 ACS
ACCESSION NUMBER:         2000:858567  CAPLUS
DOCUMENT NUMBER:          134:26053
TITLE:                      ***Oligonucleotide***   analog probe   ***arrays***
                          immobilized on solid substrates, target
                            ***nucleic***     ***acid***   analogs, and
                          probe-target improved hybridization
INVENTOR(S):              McGall, Glenn Hugh; Miyada, Charles Garrett; Cronin,
                          Maureen T.; Tan, Jennifer Dee;   ***Chee, Mark S.***
PATENT ASSIGNEE(S):       Affymetrix, Inc., USA
SOURCE:                   U.S., 35 pp., Cont.-in-part of U.S. Ser. No. 440,742,
                          abandoned.
                          CODEN: USXXAM
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   7
PATENT INFORMATION:

     PATENT NO.        KIND  DATE           APPLICATION NO.  DATE
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OTHER SOURCE(S):          MARPAT 134:26053
AB     ***Oligonucleotide***   analog   ***arrays***   attached to solid
     substrates and methods related to the use thereof are provided.  The
       ***oligonucleotide***   analogs hybridize to nucleic acids with either
     higher or lower specificity than corresponding unmodified
     oligonucleotides.  Target nucleic acids which comprise nucleotide analogs
     are bound to   ***oligonucleotide***   and   ***oligonucleotide***
     analog   ***arrays***   .  Examples include   ***oligonucleotide***   prob
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arrays synthesized using VLSIPS (very large scale immobilized polymer synthesis), [redacted]plification of ***nucle[redacted]** ***acid*** targets with incorporation of nucleotide analogs, and probe-target duplex thermostability anal.

L9 ANSWER 2 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:124057 CAPLUS
DOCUMENT NUMBER: 132:176568
TITLE: ***Arrays*** of ***nucleic*** ***acid*** probes and the detection of cystic fibrosis carriers or patients by sequencing by hybridization
INVENTOR(S): Cronin, Maureen T.; Miyada, Charles Garrett; Hubbell, Earl A.; ***Chee, Mark*** ; Fodor, Stephen P. A.; Huang, Xiaohua C.; Lipshutz, Robert J.; Lobban, Peter E.; Morris, Macdonald S.; Sheldon, Edward L.
PATENT ASSIGNEE(S): Affymetrix, Inc., USA
SOURCE: U.S., 114 pp., Cont.-in-part of U.S. Ser. No. 510,521
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 7
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
US 6027880	A	20000222	US 1995-544381	19951010	
WO 9511995	A1	19950504	WO 1994-US12305	19941026	<--
US 5837832	A	19981117	US 1995-441887	19950516	<--
US 6045996	A	20000404	US 1996-648709	19960516	
US 5861242	A	19990119	US 1997-781550	19970109	

AB Organized ***arrays*** of immobilized probes that can be used to rapidly sequence the CFTR gene and to detect mutations in carriers or in the diagnosis of patients are described. The ***arrays*** consist of several lanes, with one carrying an ***array*** of overlapping probes corresponding to the wild-type gene. The other lanes contain similar ***arrays*** of probes with their sequences systematically altered, o lane is dedicated to substitutions with one base.
REFERENCE COUNT: 20
REFERENCE(S): (1) Anon; WO 8910977 1989 CAPLUS
(2) Anon; WO 8911548 1989 CAPLUS
(3) Anon; WO 9000626 1990 CAPLUS
(4) Anon; WO 9003382 1990 CAPLUS
(5) Anon; WO 9210092 1992 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 3 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:8155 CAPLUS
DOCUMENT NUMBER: 130:62005
TITLE: Method to detect gene polymorphisms and monitor allelic expression employing a probe ***array***
INVENTOR(S): ***Chee, Mark***
PATENT ASSIGNEE(S): Affymetrix, Inc., USA
SOURCE: PCT Int. Appl., 30 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

WO 9856954	A1	19981217	WO 1998-U 442	19980611 <--	
EP 1009857	A1	20000621	EP 1998-930246	19980611	

AB The invention provides methods of monitoring expression levels of different polymorphic forms of a gene. Such methods entail analyzing genomic ***DNA*** from an individual to det. the presence of heterozygous polymorphic forms at a polymorphic site within a transcribed sequence of a gene of interest. RNA from a tissue of the individual in which the gene is expressed is then analyzed to det. relative proportions of polymorphic forms in transcripts of the gene. Having identified alleles of a gene that are expressed at different levels, the alleles can be further analyzed to locate a second polymorphism that has a causative role in the different expression levels. The methods are amenable to analyzing large collections of genes simultaneously using ***arrays*** of immobilized probes.

REFERENCE COUNT: 6

REFERENCE(S):
(1) Apple; US 5567809 A 1996 CAPLUS
(2) Cantor; US 5503980 A 1996 CAPLUS
(3) Cantor; US 5631134 A 1997 CAPLUS
(4) Cantor; US 5795714 A 1998 CAPLUS
(5) Guo, Z; Nucleic Acids Research 1994, V22(24), P5456 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 4 OF 18 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1998:801310 CAPLUS

DOCUMENT NUMBER: 130:178005

TITLE: Mutation detection by ligation to complete n-mer ***DNA*** ***arrays***

AUTHOR(S): Gunderson, Kevin L.; Huang, Xiaohua C.; Morris, Macdonald S.; Lipshutz, Robert J.; Lockhart, David J. ***Chee, Mark S.***

CORPORATE SOURCE: Affymetrix, Inc., Santa Clara, CA, 95051, USA

SOURCE: Genome Res. (***1998***), 8(11), 1142-1153
CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A new approach to comparative ***nucleic*** ***acid*** sequence anal. is described that uses the ligation of ***DNA*** targets to high-d. ***arrays*** contg. complete sets of covalently attached oligonucleotides of length eight and nine. The combination of enzymic or chem. ligation with a directed comparative anal. avoids many of the intrinsic difficulties assocd. with hybridization-based de novo sequence reconstruction methods described previously. Double-stranded ***DNA*** target were fragmented and labeled to produce quasirandom populations of 5′ termini suitable for ligation and detection on the ***arrays*** , sequences of 1.2-kb targets were verified with >99.9% accuracy. Mutation in target sequences were detected by directly comparing the intensity pattern obtained for an unknown with that obtained for a known ref. sequence. For targets of moderate length (1.2 kb), 100% of the mutations in the queried sequences were detected with 9-mer ***arrays*** . For higher complexity targets (2.5 and 16.6 kb), a relatively high percentage of mutations (90% and 66%, resp.) were correctly identified with a low false-pos. rate of <0.03 percent. The methods described provide a genera approach to analyzing ***nucleic*** ***acid*** samples on the basis of the interpretation of sequence-specific patterns of hybridizatio and ligation on complete n-mer ***oligonucleotide*** ***arrays***

REFERENCE COUNT: 24

REFERENCE(S):
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(2) Belyi, I; Comput Appl Biosci 1997, V13, P205

CAPLUS
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(4) Broude, N; Proc Natl Acad Sci 1994, V91, P3072 CAPLUS
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 5 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:640369 CAPLUS
DOCUMENT NUMBER: 129:255994
TITLE: Iterative resequencing of polynucleotides using an ***array*** of probes
INVENTOR(S): ***Chee, Mark***
PATENT ASSIGNEE(S): Affymetrix, Inc., USA
SOURCE: PCT Int. Appl., 22 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9841657	A1	19980924	WO 1998-US5451	19980319 <--

AB The invention provides iterative methods of analyzing a target ***nucleic*** ***acid*** that represents a variant of a ref. ***nucleic*** ***acid*** . An ***array*** of probes is design to be complementary to an estd. sequence of a target ***nucleic*** ***acid*** . The ***array*** of probes is then hybridized to the target ***nucleic*** ***acid*** . The target sequence is reestimated from hybridization pattern of the ***array*** to the target ***nucleic*** ***acid*** . A further ***array*** of probes is then designed to be complementary to the reestimated sequence, and this ***array*** is used to obtain a further reestimate of the sequence of the target ***nucleic*** ***acid*** . By performing iterative cycles of ***array*** design and target sequence estn., the estd. sequence of the target converges with the true sequence.

L9 ANSWER 6 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:493727 CAPLUS
DOCUMENT NUMBER: 129:118762
TITLE: Analysis of genetic polymorphisms and gene copy numbe using ***oligonucleotide*** probe ***arrays***
INVENTOR(S): Cronin, Maureen T.; Miyada, Charles G.; Hubbell, Earl A.; ***Chee, Mark*** ; Fodor, Stephen P. A.; Huang Xiaohua C.; Lipshutz, Robert J.; Lobban, Peter E.; Morris, Macdonald S.; Sheldon, Edward L.
PATENT ASSIGNEE(S): Affymetrix, Inc., USA
SOURCE: PCT Int. Appl., 114 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9830883	A2	19980716	WO 1998-US6414	19980102 <--
WO 9830883	A3	19981029		

EP 970251 A2 20000112 EP 1998-947218 19980102

AB The invention provides methods for detecting variations in polymorphic sites and/or variations in gene copy no. A no. of strategies for comparing a ***polynucleotide*** of known sequence (a ref. sequence) with variants of that sequence (target sequence) are provided. The comparison can be performed at the level of entire genomes, chromosomes, genes, exons or introns, or can focus on individual mutant sites and immediately adjacent bases. The strategies allow detection of variations such as mutations or polymorphisms, in the target sequence irresp. whethe a particular variant has previously been characterized. The strategies both define the nature of a variant and identify its location in a target sequence. The strategies employ ***arrays*** of ***oligonucleotide*** probes immobilized to a solid support (***DNA chips). Target sequences are analyzed by detg. the extent of hybridization at particular probes in the ***array*** . The strategy in selection of probes facilitates distinction between perfectly matched probes and probes showing single-base or other degrees of mismatches. Th strategies usually entails sampling each nucleotide of interest in a target sequence several times, thereby achieving a high degree of confidence in its identity. This level of confidence is further increase by sampling of adjacent nucleotides in the target sequence to nucleotides of interest. The present tiling strategies result in sequencing and comparison methods suitable for routine large-scale practice with a high degree of confidence in the sequence output. The methods are particularl useful for anal. of biotransformation genes, such as cytochromes P 450, and for screening an animal to tissue for the capacity to metabolize a drug.

L9 ANSWER 7 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:293656 CAPLUS
DOCUMENT NUMBER: 129:6733
TITLE: Polymorphisms in the human glucose-6 phosphate dehydrogenase locus
INVENTOR(S): ***Chee, Mark*** ; Fan, Jian-Bing
PATENT ASSIGNEE(S): Affymetrix, Inc., USA; Chee, Mark; Fan, Jian-Bing
SOURCE: PCT Int. Appl., 38 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9818967	A1	19980507	WO 1997-US19665	19971027 <--

AB The invention provides ***nucleic*** ***acid*** segments of the glucose-6 phosphate dehydrogenase (G6PD) locus of the human genome including polymorphic sites. Ten polymorphisms are identified in sequence-tagged sites in the human G6PD locus by hybridization to tiling ***arrays*** which did not contain repetitive Alu sequences. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and geneti anal.

L9 ANSWER 8 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:544330 CAPLUS
DOCUMENT NUMBER: 127:201011
TITLE: ***Oligonucleotide*** probe ***arrays*** immobilized on chips, computer programs for hybridization pattern comparison, and species

identification or polymorphism or mutation characterization

INVENTOR(S): Gingeras, Thomas A.; Mack, David; ***Chee, Mark*** S.*** ; Berno, Anthony J.; Stryer, Lubert; Ghan Ghassan; Wang, Ching

PATENT ASSIGNEE(S): Affymetrix, Inc., USA; Gingeras, Thomas A.; Mack, David; Chee, Mark S.; Berno, Anthony J.; Stryer, Lubert; Ghandour, Ghassan; Wang, Ching

SOURCE: PCT Int. Appl., 132 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9729212	A1	19970814	WO 1997-US2102	19970207 <--

AB This invention provides ***oligonucleotide*** -based ***arrays*** and methods for speciating and phenotyping organisms, for example, using ***oligonucleotide*** sequences based on the Mycobacterium tuberculos rpoB gene. The groups or species to which an organism belongs may be detd. by comparing hybridization patterns of target ***nucleic*** ***acid*** from the organism to hybridization patterns in a database. An example includes Mycobacterium tuberculosis gene rpoB anal. to identif mutations conferring resistance to rifampicin. A total of 25 M. tuberculosis isolates were analyzed. Seven of these were rifampicin resistant and had mutations. Other than the mutations identified, there were no polymorphisms in any of the 25 isolates. Another example include hybridization patterns (fingerprints) for 7 clin. important Mycobacteria species: M. gordonae, M. chelonae, M. kansasii, M. scrofulaceum, M. avium M. intracellulare, and M. xenopi.

L9 ANSWER 9 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:517576 CAPLUS
DOCUMENT NUMBER: 127:186611
TITLE: Determination of patterns of gene expression by hybridization against dense ordered ***arrays*** of arbitrary oligonucleotides

INVENTOR(S): Lockhart, David J.; ***Chee, Mark*** ; Gunderson, Kevin; Lai, Chaoqiang; Wodicka, Lisa; Cronin, Maureen T.; Lee, Danny; Tran, Huu M.; Matsuzaki, Hajime; McGall, Glenn H.; Barone, Anthony D.

PATENT ASSIGNEE(S): Affymetrix, Inc., USA; Lockhart, David J.; Chee, Mark Gunderson, Kevin; Lai, Chaoqiang; Wodicka, Lisa; Cronin, Maureen T.; Lee, Danny; Tran, Huu M.; et al.

SOURCE: PCT Int. Appl., 214 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9727317	A1	19970731	WO 1997-US1603	19970122 <--

OTHER SOURCE(S): MARPAT 127:186611

AB A simplified method for identifying differences in ***nucleic*** ***acid*** abundances (e.g., expression levels) between two or more samples using an ***array*** of a large no. (e.g. > 1,000) of arbitrarily selected different ***oligonucleotide*** probes where the

sequence and location of each different probe is known. ***Nucleic*** ***acid*** sample (e.g. mRNA) are hybridized to the probe ***arrays*** and the pattern of hybridization is detd. Differences i the hybridization patterns between the samples indicates differences in expression of various genes between those samples. Methods of end-labeling a ***nucleic*** ***acid*** by ligation of a labeled ***oligonucleotide*** to it is also described. These methods can be used to detect hybridization by making end-labeling of the immobilized probe dependent upon formation of a hybrid. For example, if the ***nucleic*** ***acid*** is an RNA, a labeled oligoribonucleotide can be ligated using an RNA ligase. End-labeling can also be accomplishe by with labeled nucleoside triphosphates, and attaching them to the ***nucleic*** ***acid*** using a terminal transferase.

L9 ANSWER 10 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:490277 CAPLUS
TITLE: Genomics and ***DNA*** chips.
AUTHOR(S): Lockhart, David J.; ***Chee, Mark S.***
CORPORATE SOURCE: Affymetrix, Santa Clara, CA, 95051, USA
SOURCE: Book of Abstracts, 214th ACS National Meeting, Las Vegas, NV, September 7-11 (***1997***), PHYS-115. American Chemical Society: Washington, D. C.
CODEN: 64RNAO
DOCUMENT TYPE: Conference; Meeting Abstract
LANGUAGE: English
AB The most basic characterization of a cell or an organism involves the detn. of the sequence of the genomic ***DNA*** and the expression levels of the encoded genes. We have developed the use of high-d. ***arrays*** of chem. synthesized oligonucleotides (***DNA*** chi for the characterization of genomic sequence as well as cellular patterns of gene expression. The ***arrays*** are designed based on sequence information alone, and are synthesized in situ using a combination of photolithog. and ***oligonucleotide*** chem. We currently scan tens of kilobases for mutations or polymorphisms, and quant. monitor the expression levels of thousands of genes simultaneously. Data will be presented showing the expression patterns for over 6200 genes in yeast (all designated ORFs), and over 6500 genes in humans and mouse. These approaches scale very directly, and this is enabling the amt. of sequence information obtained and the no. of mRNAs monitored to increase rapidly. We are also designing ***arrays*** based on genomic and cDNA sequence for the simultaneous monitoring of all E. coli genes, nearly half of all Drosophila genes, and roughly 50,000 human genes. Highly parallel method of this type should prove useful for exploring gene function and the mechanisms of cellular processes, as well as for finding the genes assocd with disease.

L9 ANSWER 11 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:283823 CAPLUS
DOCUMENT NUMBER: 126:260132
TITLE: Quantification of level of expression of hundreds to millions of genes using hybridization to high density synthetic ***oligonucleotide*** probe ***arrays*** immobilized on a surface
INVENTOR(S): Lockhart, David J.; Brown, Eugene L.; Wong, Gordon; ***Chee, Mark*** ; Gingeras, Thomas R.; Mittmann, Michael P.; Lipshutz, Robert J.; Fodor, Stephen P. A. Wang, Chunwei
PATENT ASSIGNEE(S): Affymax Technologies N.V., Neth.; Lockhart, David J.; Brown, Eugene L.; Wong, Gordon; Chee, Mark; Gingeras, Thomas R.; Mittmann, Michael P.; Lipshutz, Robert J.; Fodor, Stephen P. A.; Wang, Chunwei
SOURCE: PCT Int. Appl., 126 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
WO 9710365	A1	19970320	WO 1996-US14839	19960913	<--
US 6040138	A	20000321	US 1995-529115	19950915	
CA 2232047	AA	19970320	CA 1996-2232047	19960913	<--
AU 9670734	A1	19970401	AU 1996-70734	19960913	<--
EP 853679	A1	19980722	EP 1996-931598	19960913	<--

AB This invention provides methods of monitoring the expression levels of a multiplicity of genes. The methods involve hybridizing a ***nucleic*** ***acid*** sample to a high d. ***array*** of ***oligonucleotide*** probes where the high d. ***array*** contai ***oligonucleotide*** probes complementary to subsequences of target nucleic acids in the ***nucleic*** ***acid*** sample. In one embodiment, the method involves providing a pool of target nucleic acids comprising RNA transcripts of one or more target genes, or nucleic acids derived from the RNA transcripts, hybridizing said pool of nucleic acids to an ***array*** of ***oligonucleotide*** probes immobilized on surface, where the ***array*** comprising more than 100 different oligonucleotides and each different ***oligonucleotide*** is localize in a predetd. region of the surface, the d. of the different oligonucleotides is greater than about 60 different oligonucleotides per cm2, and the ***oligonucleotide*** probes are complementary to the RN transcripts or nucleic acids derived from the RNA transcripts; and quantifying the hybridized nucleic acids in the ***array*** .

L9 ANSWER 12 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:14728 CAPLUS
DOCUMENT NUMBER: 126:43598
TITLE: ***Oligonucleotide*** analog probe ***arrays*** immobilized on solid substrates, target ***nucleic*** ***acid*** analogs, and probe-target improved hybridization
INVENTOR(S): Mcgall, Glenn H.; Miyada, Charles G.; Cronin, Maureen T.; Tan, Jennifer D.; ***Chee, Mark S.***
PATENT ASSIGNEE(S): USA
SOURCE: Eur. Pat. Appl., 43 pp
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 7
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
EP 742287	A2	19961113	EP 1996-303245	19960509	<--
EP 742287	A3	19971229			
US 6156501	A	20001205	US 1996-630427	19960403	

OTHER SOURCE(S): MARPAT 126:43598
AB ***Oligonucleotide*** analog ***arrays*** attached to solid substrates and methods related to the use thereof are provided. The ***oligonucleotide*** analogs hybridize to nucleic acids with either higher or lower specificity than corresponding unmodified oligonucleotides. Target nucleic acids which comprise nucleotide analogs are bound to ***oligonucleotide*** and ***oligonucleotide***

analog ***arrays*** . Examples include ***oligonucleotide*** prob ***arrays*** synthesized using VLSIPS (very large scale immobilized polymer synthesis), amplification of ***nucleic*** ***acid*** targets with incorporation of nucleotide analogs, and probe-target duplex thermostability anal.

L9 ANSWER 13 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:749764 CAPLUS
DOCUMENT NUMBER: 126:43230
TITLE: Expression monitoring by hybridization to high-densit ***oligonucleotide*** ***arrays***
AUTHOR(S): Lockhart, David J.; Dong, Helin; Byrne, Michael C.; Follettie, Maximillian T.; Gallo, Michael V.; ***Chee, Mark S.*** ; Mittmann, Michael; Wang, Chunwei; Kobayashi, Michiko; Horton, Heidi; Brown, Eugene L.
CORPORATE SOURCE: Affymetrix, Santa Clara, CA, 95051, USA
SOURCE: Nat. Biotechnol. (***1996***), 14(13), 1675-1680
CODEN: NABIF9; ISSN: 1087-0156
PUBLISHER: Nature Publishing Co.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The human genome encodes approx. 100,000 different genes, and at least partial sequence information for nearly all will be available soon. Sequence information alone, however, is insufficient for a full understanding of gene function, expression, regulation, and splice-site variation. Because cellular processes are governed by the repertoire of expressed genes, and the levels and timing of expression, it is important to have exptl. tools for the direct monitoring of large nos. of mRNAs in parallel. We have developed an approach that is based on hybridization t small, high-d. ***arrays*** contg. tens of thousands of synthetic oligonucleotides. The ***arrays*** are designed based on sequence information alone and are synthesized in situ using a combination of photolithog. and ***oligonucleotide*** chem. RNAs present at a frequency of 1:300,000 are unambiguously detected, and detection is quant over more than three orders of magnitude. This approach provides a way t use directly the growing body of sequence information for highly parallel exptl. investigations. Because of the combinatorial nature of the chem. and the ability to synthesize small ***arrays*** contg. hundreds of thousands of specifically chosen oligonucleotides, the method is readily scalable to the simultaneous monitoring of tens of thousands of genes.

L9 ANSWER 14 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:735351 CAPLUS
DOCUMENT NUMBER: 126:15255
TITLE: Detection of heterozygous mutations in BRCA1 using high density ***oligonucleotide*** ***arrays*** and two-color fluorescence analysis
AUTHOR(S): Hacia, Joseph G.; Brody, Lawrence C.; ***Chee, Mark ***
S.*** ; Fodor, Stephen P. A.; Collins, Francis
CORPORATE SOURCE: Natl. Center Human Genome Res., Natl. Insts. Health, Bethesda, MD, 20892, USA
SOURCE: Nat. Genet. (***1996***), 14(4), 441-447
CODEN: NGENEC; ISSN: 1061-4036
PUBLISHER: Nature Publishing Co.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The ability to scan a large gene rapidly and accurately for all possible heterozygous mutations in large nos. of patient samples will be crit. for the future of medicine. We have designed high-d. ***arrays*** consisting of over 96,600 oligonucleotides 20-nucleotides (nt) in length to screen for a wide range of heterozygous mutations in the 3.45-kilobase (kb) exon 11 of the hereditary breast and ovarian cancer gene BRCA1. Ref

and test samples were co-hybridized to these ***arrays*** and differences in hybridization patterns quantitated by two-color anal. Fourteen of fifteen patient samples with known mutations were accurately diagnosed, and no false pos. mutations were identified in 20 control samples. Eight single nucleotide polymorphisms were also readily detected. ***DNA*** chip-based assays may provide a valuable new technol. for high-throughput cost-efficient detection of genetic alterations.

L9 ANSWER 15 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:641840 CAPLUS
DOCUMENT NUMBER: 125:294156
TITLE: Accessing genetic information with high-density ***DNA*** ***arrays***
AUTHOR(S): ***Chee, Mark*** ; Yang, Robert; Hubbell, Earl; Berno, Anthony; Huang, Xiaohua C.; Stern, David; Winkler, Jim; Lockhart, David J.; Morris, Macdonald S.; Fodor, Stephen P. A.
CORPORATE SOURCE: Affymetrix, Santa Clara, CA, 95051, USA
SOURCE: Science (Washington, D. C.) (***1996***), 274(5287), 610-614
CODEN: SCIEAS; ISSN: 0036-8075
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Rapid access to genetic information is central to the revolution taking place in mol. genetics. The simultaneous anal. of the entire human mitochondrial genome is described here. ***DNA*** ***arrays*** contg. up to 135,000 probes complementary to the 16.6-kilobase human mitochondrial genome were generated by light-directed chem. synthesis. A two-color labeling scheme was developed that allows simultaneous comparison of a polymorphic target to a ref. ***DNA*** or RNA. Complete hybridization patterns were revealed in a matter of minutes. Sequence polymorphisms were detected with single-base resoln. and unprecedented efficiency. The methods described are generic and can be used to address a variety of questions in mol. genetics including gene expression, genetic linkage, and genetic variability.

L9 ANSWER 16 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:458126 CAPLUS
DOCUMENT NUMBER: 125:107046
TITLE: ***Nucleic*** ***acid*** library ***arrays*** , methods for synthesizing them and methods for sequencing and sample screening using the
INVENTOR(S): Lockhart, David J.; ***Chee, Mark S.*** ; Vetter, Dirk; Diggelmann, Martin
PATENT ASSIGNEE(S): Affymax Technologies N.V., Neth. Antilles
SOURCE: Eur. Pat. Appl., 73 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 721016	A2	19960710	EP 1995-307501	19951020 <--
EP 721016	A3	19991103		
US 5556752	A	19960917	US 1994-327687	19941024 <--
US 5770722	A	19980623	US 1996-664093	19960613 <--

AB Disclosed are methods for discriminating between fully complementary hybrids and those that differ by one or more base pairs and libraries of

unimol., double-stranded oligonucleotides on a solid support. In these methods, the quality of hybridization signals on high d.
oligonucleotide ***arrays*** is improved by (1) the nucleas treatment and (2) ligation reactions. Also provided are libraries of unimol. or intermol., double-stranded oligonucleotides on a solid support These libraries are useful in pharmaceutical discovery for the screening of numerous biol. samples for specific interactions between the double-stranded oligonucleotides, and peptides, proteins, drugs and RNA. In a related aspect, the present invention provides libraries of conformationally restricted probes on a solid support. The probes are restricted in their movement and flexibility using double-stranded oligonucleotides as scaffolding. The probes are also useful in various screening procedures assocd. with drug discovery and diagnosis. The present invention further provides methods for the prepn. and screening o the above libraries.

L9 ANSWER 17 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1995:792433 CAPLUS
DOCUMENT NUMBER: 123:307444
TITLE: Using ***oligonucleotide*** probe ***arrays*** to access genetic diversity
AUTHOR(S): Lipshutz, R. J.; Morris, D.; ***Chee, M.*** ; Hubbell, E.; Kozal, M. J.; Shah, N.; Shen, N.; Yang, R.; Fodor, S. P. A.
CORPORATE SOURCE: Affymetrix, Santa Clara, CA, USA
SOURCE: BioTechniques (***1995***), 19(3), 442-7
CODEN: BTNQDO; ISSN: 0736-6205
DOCUMENT TYPE: Journal
LANGUAGE: English
AB As the Human Genome Project and related efforts identify and det. the ***DNA*** sequences of human genes, it is important that highly relia and efficient mechanisms are found to access individual genetic variation It is only through a greater understanding of genetic diversity that the true benefit of the Human Genome project will be realized. One approach, hybridization to high-d. ***arrays*** of oligonucleotides, is a fast and effective means of accessing this genetic variation. Light-directed chem. synthesis has been used to generate miniaturized, high-d. ***arrays*** of ***oligonucleotide*** probes. Application-specif ***oligonucleotide*** probe ***array*** designs have been develop for the rapid screening of characterized genes. Dedicated instrumentatio and software have been developed for ***array*** hybridization, fluorescence detection and data acquisition and anal. In a specific and challenging application, ***oligonucleotide*** probe ***arrays*** have been used to screen the reverse transcriptase and protease genes of the highly polymorphic HIV-I genome to explore genetic diversity and detect mutations conferring resistance to antiviral drugs. Results from this application strongly suggest that ***oligonucleotide*** probe ***arrays*** will be a powerful tool for rapid investigations in sequence checking pathogen detection, expression monitoring and ***DNA*** mol. recognition.

L9 ANSWER 18 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1995:713926 CAPLUS
DOCUMENT NUMBER: 123:135082
TITLE: ***Arrays*** of ***oligonucleotide*** probes immobilized on silica chips and selective ***nucleic*** ***acid*** hybridization for biochemical studies and medical diagnostics
INVENTOR(S): ***Chee, Mark*** ; Cronin, Maureen T.; Fodor, Stephen P. A.; Gingeras, Thomas R.; Huang, Xiaohua C. Hubbell, Earl A.; Lipshutz, Robert J.; Lobban, Peter E.; Miyada, Charles Garrett; et al.
PATENT ASSIGNEE(S): Affymax Technologies N.V., Neth.

SOURCE: PCT Int. Appl., 222 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 7
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9511995	A1	19950504	WO 1994-US12305	19941026 <--

AB The invention provides chips of immobilized ***oligonucleotide*** probes, and methods employing the chips, for comparing a ref. ***polynucleotide*** sequence of known sequence with a target sequenc showing substantial similarity with the ref. sequence, but differing in the presence of e.g., mutations. Human immunodeficiency virus genes, cystic fibrosis genes, and the human mitochondrial genome exemplify uses of the methods.

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L10           8 STUELPNAGEL J?/AU

=> s l10 and (dna or nucleic acid or oligonucleotide or polynucleotide)
        505849 DNA
        106500 NUCLEIC
       2955456 ACID
         69613 NUCLEIC ACID
                 (NUCLEIC(W)ACID)
         34173 OLIGONUCLEOTIDE
          8811 POLYNUCLEOTIDE
L11           4 L10 AND (DNA OR NUCLEIC ACID OR OLIGONUCLEOTIDE OR POLYNUCLEOTI
                E)

=> s l11 and array?
         74102 ARRAY?
L12           3 L11 AND ARRAY?

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      17442092 PY<1999
L13           0 L12 AND PY<1999



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         16769 MICROSPHERE?
          8922 MICROPARTICLE?
L1       25074 MICROSPHERE? OR MICROPARTICLE?

=> s l1 (p) array?
         74102 ARRAY?
L2         172 L1 (P) ARRAY?

=> s l2 (p) tag?
         26600 TAG?
L3            3 L2 (P) TAG?
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L3 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2001:152872 CAPLUS
DOCUMENT NUMBER: 134:203076
TITLE: Liquid array technology
INVENTOR(S): Chandler, Mark B.
PATENT ASSIGNEE(S): Luminex Corporation, USA
SOURCE: PCT Int. Appl., 62 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001014589	A2	20010301	WO 2000-US22769	20000821

L3 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:474214 CAPLUS
DOCUMENT NUMBER: 131:171701
TITLE: Spherical cellulose. Crosslinking of epichlorohydrin
AUTHOR(S): Bordallo, E.; Sabatier, J.; Bermello, A.; Cabrera, M.
CORPORATE SOURCE: Union de Investigacion Produccion de la celulosa del Bagazo UIP, Havana, Cuba
SOURCE: Rev. Deriv. Cana Azucar (1998), 32(3), 84-90
CODEN: SDCAAR; ISSN: 1025-3076
PUBLISHER: Instituto Cubano de Investigaciones de los Derivados de la Cana de Azucar
DOCUMENT TYPE: Journal; (computer magnetic disk)
LANGUAGE: Spanish
REFERENCE COUNT: 17
REFERENCE(S): (4) Buschle-Diller, G; Cellulose 1995, V2(3), P179 CAPLUS
(6) Dautzenberg, H; Cell Chem Technol 1980, V14(5), P633 CAPLUS
(9) Kuniak, L; Cellulose Chem Technol 1974, V8(3), P247 CAPLUS
(12) Okuma, S; US 5064950 1991 CAPLUS
(14) Porath, J; J Chromatogr 1971, V60(2), P167 CAPLU
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:268797 CAPLUS
DOCUMENT NUMBER: 131:70544
TITLE: In Situ Assembly of Colloidal Particles into Miniaturized Biosensors
AUTHOR(S): Velev, O. D.; Kaler, E. W.
CORPORATE SOURCE: Center for Molecular and Engineering Thermodynamics Department of Chemical Engineering, University of Delaware, Newark, DE, 19716, USA
SOURCE: Langmuir (1999), 15(11), 3693-3698
CODEN: LANGD5; ISSN: 0743-7463
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 43
REFERENCE(S): (7) Braun, E; Nature 1998, V391, P775 CAPLUS
(8) Burmeister, F; Adv Mater 1998, V10, P495 CAPLUS
(9) Chiruvolu, S; Science 1994, V264, P1753 CAPLUS
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